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Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2007; month=12; day=3; hr=14; min=40; sec=4; ms=272;]
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Application No: 10088202   Version No: 5.0

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Started: 2007-11-09 21:52:50.818

Finished: 2007-11-09 21:52:51.154

Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 336 ms

Total Warnings: 2

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No. of SeqIDs Defined: 6

Actual SeqID Count: 6

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<110>   Mogam Biotechnology Research Institute
        Park, Eun Jeong
        Kim, Jang Seong
        Jang, Jihoon
        Yum, Jungsun
        Chung, Soo-il

<120>   Novel Detoxified Mutants of Escherichia coli Heat-Labile
        Enterotoxin

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<140>   10088202
<141>   2002-03-15

<150>   PCT/KR99/00555
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<170>   PatentIn version 3.4

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Tyr Ala Asn Gly Asp Arg Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp
                20   25   30

Glu Ile Lys Arg Ser Gly Gly Leu Met Pro Arg Gly His Asn Glu Tyr
            35   40   45

Phe Asp Arg Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg
    50   55   60

Gly Thr Gln Thr Gly Phe Val Arg Tyr Asp Asp Gly Tyr Val Ser Thr
65   70   75   80

Tyr Leu Ser Leu Arg Ser Ala His Leu Ala Gly Gln Ser Ile Leu Ser
                85   90   95

Gly Tyr Ser Thr Tyr Tyr Ile Tyr Val Ile Ala Thr Ala Pro Asn Met
                100   105   110

Phe Asn Val Asn Asp Val Leu Gly Val Tyr Ser Pro His Pro Tyr Glu
            115   120   125

Gln Glu Val Ser Ala Leu Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly
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Trp Tyr Arg Val Asn Phe Gly Val Ile Asp Glu Arg Leu His Arg Asn
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Arg Glu Tyr Arg Asp Arg Tyr Tyr Arg Asn Leu Asn Ile Ala Pro Ala
                165   170   175

Glu Asp Gly Tyr Arg Leu Ala Gly Phe Pro Pro Asp His Gln Ala Trp
            180   185   190

Arg Glu Glu Pro Trp Ile His His Ala Pro Gln Gly Cys Gly Asn Ser
            195   200   205

Ser Arg Thr Ile Thr Gly Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu
    210   215   220

Ser Thr Ile Tyr Leu Arg Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile
225   230   235   240

Phe Ser Asp Tyr Gln Ser Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp
            245   250   255

Glu Leu Met Asn Lys Val Lys Phe Tyr Val Leu Phe Thr Ala Leu Leu
            260   265   270

Ser Ser Leu Cys Ala His Gly Ala Pro Gln Ser Ile Thr Glu Leu Cys
            275   280   285

Ser Glu Tyr His Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys Ile Leu
            290   295   300

Ser Tyr Thr Glu Ser Met Ala Gly Lys Arg Glu Met Val Ile Ile Thr
305   310   315   320

Phe Lys Ser Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln His
            325   330   335

Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg
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Ile Thr Tyr Leu Thr Glu Thr Lys Ile Asp Lys Leu Cys Val Trp Asn
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Asn Lys Thr Pro Asn Ser Ile Ala Ala Ile Ser Met Glu Asn
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acaaaccggc tttgtcagat atgatgacgg atatgtttcc acttacctta gtttgagaag     420

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tggaataata aaaccccaa ttcaattgcg gcaatcagta tggaaaacta gtttgcttta     1320

aaagcatgtc taatgctagg aacctatata acaactactg tacttatact aatgagcctt    1380

atgctgcatt tgaaaaggcg gtagaggatg caataccgat ccttaaactg taacactata    1440

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<212> PRT
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Met Lys Asn Ile Thr Phe Ile Phe Phe Ile Leu Leu Ala Ser Pro Leu
1   5   10   15

Tyr Ala Asn Gly Asp Arg Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp
                20   25   30

Glu Ile Lys Arg Ser Gly Gly Leu Met Pro Arg Gly His Asn Glu Tyr
                35   40   45

Phe Asp Arg Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg
    50   55   60

Gly Thr Gln Thr Gly Phe Val Arg Tyr Asp Asp Gly Tyr Val Ser Thr
65   70   75   80

Ser Leu Ser Leu Arg Ser Ala His Leu Ala Gly Gln Ser Ile Leu Ser
                85   90   95

Gly Tyr Ser Thr Tyr Tyr Ile Tyr Val Ile Ala Thr Ala Pro Asn Met
                100   105   110

Phe Asn Val Asn Asp Val Leu Gly Val Tyr Ser Pro His Pro Tyr Gln
            115   120   125

Val Ser Ala Leu Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr
    130   135   140

Arg Val Asn Phe Gly Val Ile Asp Glu Arg Leu His Arg Asn Arg Glu
145   150   155   160

Tyr Arg Asp Arg Tyr Tyr Arg Asn Leu Asn Ile Ala Pro Ala Glu Asp
                165   170   175

Gly Tyr Arg Leu Ala Gly Phe Pro Pro Asp His Gln Ala Trp Arg Glu
                180   185   190

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Glu Pro Trp Ile His His Ala Pro Gln Gly Cys Gly Asn Ser Ser Arg
        195                 200                 205

Thr Ile Thr Gly Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu Ser Thr
        210                 215                 220

Ile Tyr Leu Arg Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser
225                 230                 235                 240

Asp Tyr Gln Ser Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp Glu Leu
                245                 250                 255

Met Asn Lys Val Lys Phe Tyr Val Leu Phe Thr Ala Leu Leu Ser Ser
            260                 265                 270

Leu Cys Ala His Gly Ala Pro Gln Ser Ile Thr Glu Leu Cys Ser Glu
        275                 280                 285

Tyr His Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys Ile Leu Ser Tyr
        290                 295                 300

Thr Glu Ser Met Ala Gly Lys Arg Glu Met Val Ile Ile Thr Phe Lys
305                 310                 315                 320

Ser Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp
                325                 330                 335

Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Thr
            340                 345                 350

Tyr Leu Thr Glu Thr Lys Ile Asp Lys Leu Cys Val Trp Asn Asn Lys
        355                 360                 365

Thr Pro Asn Ser Ile Ala Ala Ile Ser Met Glu Asn
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catttttttt attttattag catcgccatt atatgcaaat ggcgacagat tataccgtgc      240

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tgagtacttc gatagaggaa ctcaaatgaa tattaatctt tatgatcacg cgagaggaac      360

acaaaccggc tttgtcagat atgatgacgg atatgtttcc acttctctta gtttgagaag      420

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acggcgttac tatcctctct atgtgcacac ggagctcctc agtctattac agaactatgt     1020

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